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SEQUENCE LISTING

<110> Baell, Jonathan  
Huang, David  
Smith, Brian J  
Street, Ian P

<120> Peptides and Therapeutic Uses Therefor

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<140> US 10/540,390  
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 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 17

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 18  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 18

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 18

Ile Ala Lys Xaa Leu Ala Lys Ile Gly Asp Xaa Phe  
 1 5 10

<210> 19  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 19

<220>  
 <221> MISC\_FEATURE  
 <222> (5)..(5)  
 <223> X = any amino acid residue, wherein it is linked to residue 12 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (12)..(12)  
 <223> X = any amino acid residue, wherein it is linked to residue 5 by  
 a linker

<400> 19

Lys Tyr Ala Lys Xaa Leu Ala Lys Ile Gly Asp Xaa Phe  
 1 5 10

<210> 20  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 20

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 20

Tyr Gly Arg Xaa Leu Arg Arg Met Ser Asp Xaa Phe  
 1 5 10

<210> 21  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 21

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

&lt;400&gt; 21

Ile Ala Arg Xaa Leu Ala Gln Val Gly Asp Xaa Met  
 1 5 10

<210> 22  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 22

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

&lt;400&gt; 22

Val Gly Arg Xaa Leu Ala Ile Ile Gly Asp Xaa Ile  
 1 5 10

<210> 23  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 23

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

&lt;400&gt; 23

Ile Ala Gln Xaa Leu Ser Ser Ile Gly Ser Xaa Phe  
 1 5 10

<210> 24  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 24

<220>  
 <221> MOD\_RES  
 <222> (2)..(2)  
 <223> Aib

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 24

Ile Xaa Gln Xaa Leu Arg Arg Ile Ala Asp Xaa Phe  
 1 5 10

<210> 25  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 25

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 25

Tyr Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 26  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 26

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 26

Ala Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 27  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 27

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 27

Ile Ala Gln Xaa Ala Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 28  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 28

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 28

Ile Ala Gln Xaa Leu Arg Arg Ala Gly Asp Xaa Ala  
 1 5 10

<210> 29  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 29

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 29

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 30  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 30

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE

<222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 30

Ile Ala Gln Xaa Leu Ser Ser Ile Gly Asp Xaa Phe  
 1 5 10

<210> 31  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 31

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 31

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe Asn Ala Ser Phe  
 1 5 10 15

<210> 32  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 32

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 a linker

<400> 32

Lys Ile Ala Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10



<210> 33  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 33

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> X = any amino acid residue, wherein it is linked to residue 8 by  
 linker NH(CH<sub>2</sub>)<sub>5</sub>NH

<220>  
 <221> MISC\_FEATURE  
 <222> (8)..(8)  
 <223> X = any amino acid residue, wherein it is linked to residue 1 by  
 linker NH(CH<sub>2</sub>)<sub>5</sub>NH

<400> 33

Xaa Ile Ala Gln Glu Leu Arg Xaa Ile Gly Asp Glu Phe  
 1 5 10

<210> 34  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 34

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 linker NH(CH<sub>2</sub>)<sub>5</sub>NH

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 linker NH(CH<sub>2</sub>)<sub>5</sub>NH

<400> 34

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 35  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 35

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 linker NH(CH<sub>2</sub>)<sub>6</sub>NH

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 linker NH(CH<sub>2</sub>)<sub>6</sub>NH

<400> 35

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 36  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 36

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> X = any amino acid residue, wherein it is linked to residue 11 by  
 linker NHCH<sub>2</sub>CONH(CH<sub>2</sub>)<sub>2</sub>NH

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> X = any amino acid residue, wherein it is linked to residue 4 by  
 linker NHCH<sub>2</sub>CONH(CH<sub>2</sub>)<sub>2</sub>NH

<400> 36

Ile Ala Gln Xaa Leu Arg Arg Ile Gly Asp Xaa Phe  
 1 5 10

<210> 37  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 37

<400> 37

Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn  
 1 5 10

<210> 38  
 <211> 26  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 38

<400> 38

Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly  
1 5 10 15

Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg  
20 25

<210> 39

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 39

<400> 39

Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn  
1 5 10

<210> 40

<211> 26

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 40

<220>

<221> MOD\_RES

<222> (1)..(1)

<223> Biotinylation

<400> 40

Asp Leu Arg Pro Glu Ile Arg Ile Ala Gln Glu Leu Arg Arg Ile Gly  
1 5 10 15

Asp Glu Phe Asn Glu Thr Tyr Thr Arg Arg  
20 25

<210> 41

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Peptide 41

<400> 41

Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe  
 1 5 10

<210> 42  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 42

<400> 42

Gln Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe  
 1 5 10

<210> 43  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 43

<220>  
 <221> MISC\_FEATURE  
 <222> (1)..(1)  
 <223> linked to residue 8 by a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (8)..(8)  
 <223> linked to residue 1 by a linker

<400> 43

Glx Ile Ala Gln Glu Leu Arg Glx Ile Gly Asp Glu Phe  
 1 5 10

<210> 44  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 44

<220>  
 <221> MISC\_FEATURE  
 <222> (4)..(4)  
 <223> linked to residue 11 by a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (11)..(11)  
 <223> linked to residue 4 by a linker

<400> 44

Ile Ala Gln Glx Leu Arg Arg Ile Gly Asp Glx Phe  
 1 5 10

<210> 45  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 45

<400> 45

Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe  
 1 5 10

<210> 46  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 46

<220>  
 <221> MISC\_FEATURE  
 <222> (2)..(2)  
 <223> linked to 9 by a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (9)..(9)  
 <223> linked to 2 by a linker

<400> 46

Ile Glx Ile Ala Gln Glu Leu Arg Glx Ile Gly Asp Glu Phe Asn Ala  
 1 5 10 15

<210> 47  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Peptide 47

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> linked to residue 13 by a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (13)..(13)  
 <223> linked to residue 6 by a linker

&lt;400&gt; 47

Ile Trp Ile Ala Gln Glx Leu Arg Arg Ile Gly Asp Glx Phe Asn Ala  
 1 5 10 15

&lt;210&gt; 48

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide 48

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (9)..(9)

&lt;223&gt; linked to residue 16 by a linker

&lt;220&gt;

&lt;221&gt; MISC\_FEATURE

&lt;222&gt; (16)..(16)

&lt;223&gt; linked to residue 9 by a linker

&lt;400&gt; 48

Ile Trp Ile Ala Gln Glu Leu Arg Glx Ile Gly Asp Glu Phe Asn Glx  
 1 5 10 15

&lt;210&gt; 49

&lt;211&gt; 13

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide 49

&lt;400&gt; 49

Glu Ile Ala Gln Glu Leu Arg Glu Ile Gly Asp Glu Phe  
 1 5 10

&lt;210&gt; 50

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Peptide 49

&lt;400&gt; 50

Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Ala  
 1 5 10 15

&lt;210&gt; 51

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>  
 <223> G (constrained)

<220>  
 <221> MISC\_FEATURE  
 <222> (6)..(6)  
 <223> linked to residue 13 by a linker

<220>  
 <221> MISC\_FEATURE  
 <222> (13)..(13)  
 <223> linked to residue 6 by a linker

<400> 51

Gln Ala Ile Ala Gln Glx Leu Arg Arg Ile Gly Asp Glx Phe Asn Ala  
 1 5 10 15

<210> 52  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> H (linear)

<400> 52

Ile Trp Ile Ala Gln Gln Leu Arg Arg Ile Gly Asp Gln Phe Asn Ala  
 1 5 10 15

<210> 53  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> I (linear)

<400> 53

Ile Trp Ala Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Ala  
 1 5 10 15

<210> 54  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> J (linear)

<400> 54

Ile Trp Ile Ala Gln Glu Ala Arg Arg Ile Gly Asp Glu Phe Asn Ala  
 1 5 10 15

<210> 55  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> K (linear)

<400> 55

Ile Trp Ile Ala Gln Glu Leu Arg Arg Ala Gly Asp Glu Phe Asn Ala  
 1 5 10 15

<210> 56  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> L (linear)

<400> 56

Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Ala Asn Ala  
 1 5 10 15

<210> 57  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> M (linear)

<400> 57

Ile Trp Ala Ala Gln Glu Ala Arg Arg Ala Gly Asp Glu Ala Asn Ala  
 1 5 10 15

<210> 58  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> N (linear)

<400> 58

Ile Phe Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Ala  
 1 5 10 15

<210> 59  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> O (linear)



&lt;400&gt; 59

Ala	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Asn	Ala
1				5					10					15	

&lt;210&gt; 60

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; P (linear)

&lt;400&gt; 60

Ile	Ala	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Asn	Ala
1				5					10					15	

&lt;210&gt; 61

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Q (linear)

&lt;400&gt; 61

Ile	Arg	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Asn	Ala
1				5					10					15	

&lt;210&gt; 62

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; R (linear)

&lt;400&gt; 62

Ile	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Ala	Asn
1				5					10					15	

&lt;210&gt; 63

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; S (linear)

&lt;400&gt; 63

Ile	Trp	Ile	Ala	Gln	Glu	Leu	Arg	Arg	Ile	Gly	Asp	Glu	Phe	Ala	Ala
1				5					10					15	

<210> 64  
 <211> 20  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> T (linear)

<400> 64

Ile Trp Ile Ala Gln Glu Leu Cys Ile Thr Cys Ile Thr Ile Gly Asp  
 1 5 10 15

Glu Phe Asn Ala  
 20

<210> 65  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> U (linear)

<400> 65

Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly Asp Glu Phe Asn Asn  
 1 5 10 15

<210> 66  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Puma

<400> 66

Arg Glu Ile Gly Ala Gln Leu Arg Arg Met Ala Asp Asp Leu Asn Ala  
 1 5 10 15

<210> 67  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Bmf

<400> 67

Val Gln Ile Ala Arg Lys Leu Gln Ala Ile Ala Asp Gln Phe His Arg  
 1 5 10 15

<210> 68  
 <211> 26  
 <212> PRT

<213> Artificial Sequence

<220>

<223> hsBimL/Bod (81-106)

<400> 68

Asp Met Arg Pro Glu Ile Trp Ile Ala Gln Glu Leu Arg Arg Ile Gly  
1 5 10 15

Asp Glu Phe Asn Ala Tyr Tyr Ala Arg Arg  
20 25

<210> 69

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Retro inverso peptide

<400> 69

Ala Asn Phe Glu Asp Gly Ile Arg Arg Leu Glu Gln Ala Ile Trp Ile  
1 5 10 15